## Sheet 1 of 7 SELECTION SYSTEMS FOR GENETICALLY MODIFIED CELLS DOCKET NO. 257 CLLEN ENNIMAN WHITE & WICAULIFFE LLP

C. ...UELLER FURMAN MUNEE . MONTH PER . . . . . .

## DOCKET NO. 24751-2502

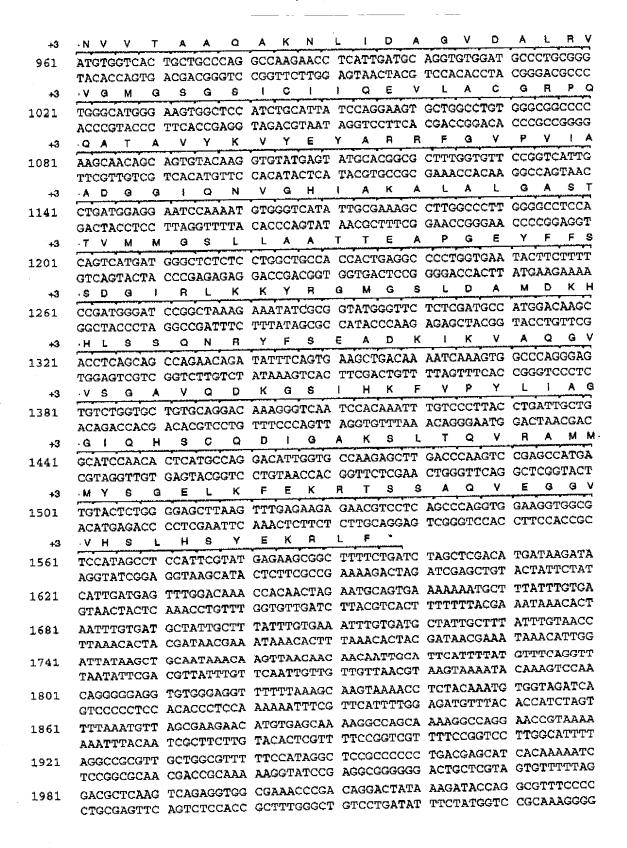
Applicant: Jensen Filed: April 30, 2001

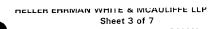
+3						M A D
1	CACCGGGGAA	GGAGGATCGA	ATTCCTGCAG	CCCGCTATCT	GCAGGCCGCC	ACCATGGCCG
-	GTGGCCGCTT	CCTCCTAGCT	TAAGGACGTC	GGGCGATAGA	CGTCCGGCGG	TGGTACCGGC
+3	·D Y L I		T S Y			AQQL
61	ACTACCTGAT	TAGTGGGGGC	ACGTCCTACG	TGCCAGACGA	CGGACTCACA	GCACAGCAGC
V-1	TGATGGACTA	ATCACCCCCG	TGCAGGATGC	ACGGTCTGCT	GCCTGAGTGT	CGTGTCGTCG
+3	L F N C	G D G		N D F L		GYID
121	TOTTO A ACTO	CCCACACGC	СТСАССТАСА	ATGACTTTCT	CATTCTCCCT	GGGTACATCG
121	ACA ACTTGAC	GCCTCTGCCG	GAGTGGATGT	TACTGAAAGA	GTAAGAGGGA	CCCATGTAGC
+3	D F T A			SALT		TLKT
		አለ አርር አርርጥር	CACCTCACTT	CTGCTCTGAC	CAAGAAAATC	ACTCTTAAGA
181	TO A ACTICACTION	TOTOCTOCAC	CTGGACTGAA	GACGAGACTG	GTTCTTTTAG	TGAGAATTCT
+3	T P L V			VTEA		IAMA
			MOGACACAG	TCACAGAGGC	TGGGATGGCC	ATAGCAATGG
241	CCCCACTGGT	ANCONCIOCO	TACCTCTCTCTC	AGTGTCTCCG	ACCCTACCGG	TATCGTTACC
	.A I T G	_		H N C T		QANE
+3					ACCTGAATTC	CAGGCCAATG
301	CGCTTACAGG	CGGTATTGGC	ANCENCACC	WCWWC TRING	TGGACTTAAG	GTCCGGTTAC
				G F I T		V L S P
+3	EV R K	• ••			AGACCCTGTG	GTCCTCAGCC
361	AAGTTCGGAA	AGTGAAGAAA	TATGAACAGG	CMANCAC	TCTGGGACAC	CAGGAGTCGG
_		_		A K A R		
+3	PKDR					,
421	CCAAGGATCG	CGTGCGGGAT	GTTTTTGAGG	CCAAGGCCCG	GCATGGTTTC	ACCCCATACC
	GGTTCCTAGC	GCACGCCCTA	CAAAAACTCC	GGTTCCGGGC	CGTACCAAAG	Veneceuration
				p 1 V 6	1 I S	SRDI
+3	.PIT D		M G S			
+3 481	CAATCACAGA	CACAGGCCGG	ATGGGGAGCC	GCTTGGTGGG	CATCATCTCC	TCCAGGGACA
481	CAATCACAGA GTTAGTGTCT	CACAGGCCGG GTGTCCGGCC	ATGGGGAGCC TACCCCTCGG	GCTTGGTGGG CGAACCACCC	CATCATCTCC CTAGTAGAGG	TCCAGGGACA
	CAATCACAGA GTTAGTGTCT	CACAGGCCGG GTGTCCGGCC K E E	ATGGGGAGCC TACCCCTCGG E H D	GCTTGGTGGG CGAACCACCC C F L E	CATCATCTCC CTAGTAGAGG E   M	TCCAGGGACA AGGTCCCTGT T K R E
481	CAATCACAGA GTTAGTGTCT .1 D F L	CACAGGCCGG GTGTCCGGCC K E E	ATGGGGAGCC TACCCCTCGG E H D GAACATGACT	GCTTGGTGGG CGAACCACCC C F L E	CATCATCTCC CTAGTAGAGG E   M AGAGATAATG	TCCAGGGACA AGGTCCCTGT T K R E ACAAAGAGGG
481 +3	CAATCACAGA GTTAGTGTCT .I D F L TTGATTTTCT AACTAAAAGA	CACAGGCCGG GTGTCCGGCC K E E CAAAGAGGAG GTTTCTCCTC	ATGGGGAGCC TACCCCTCGG E H D GAACATGACT CTTGTACTGA	GCTTGGTGGG CGAACCACCC C F L E GTTTCTTGGA CAAAGAACCT	CATCATCTCC GTAGTAGAGG E   M AGAGATAATG TCTCTATTAC	TCCAGGGACA AGGTCCCTGT T K R E ACAAAGAGGG TGTTTCTCCC
481 +3	CAATCACAGA GTTAGTGTCT .i D F L TTGATTTTCT AACTAAAAGA .E D L V	CACAGGCCGG GTGTCCGGCC K E E CAAAGAGGAG GTTTCTCCTC V A P	ATGGGGAGCC TACCCCTCGG E H D GAACATGACT CTTGTACTGA A G !	GCTTGGTGGG CGAACCACCC C F L E GTTTCTTGGA CAAAGAACCT T L K E	CATCATCTCC GTAGTAGAGG E	TCCAGGGACA AGGTCCCTGT T K R E ACAAAGAGGG TGTTTCTCCC I L Q R
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481 +3 541 +3	CAATCACAGA GTTAGTGTCT  .1 D F L  TTGATTTTCT AACTAAAAGA .E D L V  AAGACTTGGT TTCTGAACCA	CACAGGCCGG GTGTCCGGCC K E E CAAAGAGGAG GTTTCTCCTC V A P GGTAGCCCCT CCATCGGGGA	ATGGGGAGCC TACCCCTCGG E H D GAACATGACT CTTGTACTGA A G ! GCAGGCATCA CGTCCGTAGT	GCTTGGTGGG CGAACCACCC C F L E GTTTCTTGGA CAAAGAACCT T L K E CACTGAAGGA GTGACTTCCT	CATCATCTCC GTAGTAGAGG E   M AGAGATAATG TCTCTATTAC A N E GGCAAATGAA CCGTTTACTT	TCCAGGGACA AGGTCCCTGT T K R E ACAAAGAGGG TGTTTCTCCC I L Q R ATTCTGCAGC TAAGACGTCG
481 +3 541 +3	CAATCACAGA GTTAGTGTCT .I D F L TTGATTTTCT AACTAAAAGA .E D L V AAGACTTGGT TTCTGAACCA .R S K K	CACAGGCCGG GTGTCCGGCC K E E CAAAGAGGAG GTTTCTCCTC V A P GGTAGCCCCT CCATCGGGGA G K L	ATGGGGAGCC TACCCCTCGG E H D GAACATGACT CTTGTACTGA A G ! GCAGGCATCA CGTCCGTAGT P ! V	GCTTGGTGGG CGAACCACCC C F L E GTTTCTTGGA CAAAGAACCT T L K E CACTGAAGGA GTGACTTCCT N E D E	CATCATCTCC GTAGTAGAGG E   M AGAGATAATG TCTCTATTAC A N E GGCAAATGAA CCGTTTACTT E L V	TCCAGGGACA AGGTCCCTGT T K R E ACAAAGAGGG TGTTTCTCCC I L Q R ATTCTGCAGC TAAGACGTCG A I I A
481 +3 541 +3 601	CAATCACAGA GTTAGTGTCT .I D F L TTGATTTTCT AACTAAAAGA .E D L V AAGACTTGGT TTCTGAACCA .R S K K	CACAGGCCGG GTGTCCGGCC K E E CAAAGAGGAG GTTTCTCCTC V A P GGTAGCCCCT CCATCGGGGA G K L	ATGGGGAGCC TACCCCTCGG E H D GAACATGACT CTTGTACTGA A G ! GCAGGCATCA CGTCCGTAGT P ! V	GCTTGGTGGG CGAACCACCC C F L E GTTTCTTGGA CAAAGAACCT T L K E CACTGAAGGA GTGACTTCCT N E D E ATGAAGATGA	CATCATCTCC GTAGTAGAGG E   M AGAGATAATG TCTCTATTAC A N E GGCAAATGAA CCGTTTACTT E L V TGAGCTTGTG	TCCAGGGACA AGGTCCCTGT T K R E ACAAAGAGGG TGTTTCTCCC I L Q R ATTCTGCAGC TAAGACGTCG A I I A GCCATCATTG
481 +3 541 +3 601 +3	CAATCACAGA GTTAGTGTCT .I D F L TTGATTTTCT AACTAAAAGA .E D L V AAGACTTGGT TTCTGAACCA .R S K K GCAGCAAGAA CGTCGTTCTT	CACAGGCCGG GTGTCCGGCC K E E CAAAGAGAGGGG GTTTCTCCTC V A P GGTAGCCCCT CCATCGGGGA G K L GGGAAAGTTG CCCTTTCAAC	ATGGGGAGCC TACCCCTCGG E H D GAACATGACT CTTGTACTGA A G ! GCAGGCATCA CGTCCGTAGT P ! V CCCATTGTAA GGGTAACATT	GCTTGGTGGG CGAACCACCC C F L E GTTTCTTGGA CAAAGAACCT T L K E CACTGAAGGA GTGACTTCCT N E D E ATGAAGATGA TACTTCTACT	CATCATCTCC GTAGTAGAGG E   M AGAGATAATG TCTCTATTAC A N E GGCAAATGAA CCGTTTACTT E L V TGAGCTTGTG ACTCGAACAC	TCCAGGGACA AGGTCCCTGT T K R E ACAAAGAGGG TGTTTCTCCC I L Q R ATTCTGCAGC TAAGACGTCG A I I A GCCATCATTG CGGTAGTAAC
481 +3 541 +3 601 +3	CAATCACAGA GTTAGTGTCT .I D F L TTGATTTTCT AACTAAAAGA .E D L V AAGACTTGGT TTCTGAACCA .R S K K GCAGCAAGAA CGTCGTTCTT	CACAGGCCGG GTGTCCGGCC K E E CAAAGAGGAG GTTTCTCCTC V A P GGTAGCCCCT CCATCGGGGA G K L GGGAAAGTTG CCCTTTCAAC L K K	ATGGGGAGCC TACCCCTCGG E H D GAACATGACT CTTGTACTGA A G ! GCAGGCATCA CGTCCGTAGT P ! V CCCATTGTAA GGGTAACATT N R D	GCTTGCTGGG CGAACCACCC C F L E GTTTCTTGGA CAAAGAACCT T L K E CACTGAAGGA GTGACTTCCT N E D E ATGAAGATGA TACTTCTACT Y P L A	CATCATCTCC GTAGTAGAGG E   M AGAGATAATG TCTCTATTAC A N E GGCAAATGAA CCGTTTACTT E L V TGAGCTTGTG ACTCGAACAC S K D	TCCAGGGACA AGGTCCCTGT T K R E ACAAAGAGGG TGTTTCTCCC I L Q R ATTCTGCAGC TAAGACGTCG A I I A GCCATCATTG CGGTAGTAAC A K K Q
481 +3 541 +3 601 +3 661	CAATCACAGA GTTAGTGTCT .I D F L TTGATTTTCT AACTAAAAGA .E D L V AAGACTTGGT TTCTGAACCA .R S K K GCAGCAAGAA CGTCGTTCTT .A R I D	CACAGGCCGG GTGTCCGGCC K E E CAAAGAGAGGGG GTTTCTCCTC V A P GGTAGCCCCT CCATCGGGGA G K L GGGAAAGTTG CCCTTTCAAC L K K	ATGGGGAGCC TACCCCTCGG E H D GAACATGACT CTTGTACTGA A G ! GCAGGCATCA CGTCCGTAGT P ! V CCCATTGTAA GGGTAACATT N R D	GCTTGGTGGG CGAACCACCC C F L E GTTTCTTGGA CAAAGAACCT T L K E CACTGAAGGA GTGACTTCCT N E D E ATGAAGATGA TACTTCTACT Y P L A	CATCATCTCC GTAGTAGAGG E   M AGAGATAATG TCTCTATTAC A N E GGCAAATGAA CCGTTTACTT E L V TGAGCTTGTG ACTCGAACAC S K D CTCCAAAGAT	TCCAGGGACA AGGTCCCTGT T K R E ACAAAGAGGG TGTTTCTCCC I L Q R ATTCTGCAGC TAAGACGTCG A I I A GCCATCATTG CGGTAGTAAC A K K Q GCCAAGAAAC
481 +3 541 +3 601 +3 661 +3	CAATCACAGA GTTAGTGTCT .I D F L TTGATTTTCT AACTAAAAGA .E D L V AAGACTTGGT TTCTGAACCA .R S K K GCAGCAAGAA CGTCGTTCTT .A R I D CCCGGACAGA	CACAGGCCGG GTGTCCGGCC K E E CAAAGAGGAG GTTTCTCCTC V A P GGTAGCCCCT CCATCGGGGA G K L GGGAAAGTTG CCCTTTCAAC L K K CCTGAAGAAC	ATGGGGAGCC TACCCCTCGG E H D GAACATGACT CTTGTACTGA A G ! GCAGGCATCA CGTCCGTAGT P ! V CCCATTGTAA GGGTAACATT N R D AATCGGGACT TTAGCCCTGA	GCTTGGTGGG CGAACCACCC C F L E GTTTCTTGGA CAAAGAACCT T L K E CACTGAAGGA GTGACTTCCT N E D C ATGAAGATGA TACTTCTACT Y P L A ACCCACTAGC TGGGTGATCG	CATCATCTCC GTAGTAGAGG E   M  AGAGATAATG TCTCTATTAC A N E  GGCAAATGAA CCGTTTACTT E L V  TGAGCTTGTG ACTCGAACAC S K D  CTCCAAAGAT GAGGTTTCTA	TCCAGGGACA AGGTCCCTGT T K R E ACAAAGAGGG TGTTTCTCCC I L Q R ATTCTGCAGC TAAGACGTCG A I I A GCCATCATTG CGGTAGTAAC A K K Q GCCAAGAAAC CGGTTCTTTG
481 +3 541 +3 601 +3 661 +3	CAATCACAGA GTTAGTGTCT .I D F L TTGATTTTCT AACTAAAAGA .E D L V AAGACTTGGT TTCTGAACCA .R S K K GCAGCAAGAA CGTCGTTCTT .A R I D CCCGGACAGA GGGCCTGTCT .Q L L C	CACAGGCCGG GTGTCCGGCC K E E CAAAGAGGAG GTTTCTCCTC V A P GGTAGCCCCT CCATCGGGGA G K L GGGAAAGTTG CCCTTTCAAC L K K CCTGAAGAAC GGACTTCTTC G A A	ATGGGGAGCC TACCCTCGG E H D GAACATGACT CTTGTACTGA A G ! GCAGGCATCA CGTCCGTAGT P ! V CCCATTGTAA GGGTAACATT N R D AATCGGGACT TTAGCCCTGA	GCTTGGTGGG CGAACCACCC C F L E GTTTCTTGGA CAAAGAACCT T L K E CACTGAAGGA GTGACTTCCT N E D E ATGAAGATGA TACTTCTACT Y P L A ACCCACTAGC TGGGTGATCG H E D C	CATCATCTCC GTAGTAGAGG E   M  AGAGATAATG TCTCTATTAC A N E GGCAAATGAA CCGTTTACTT E L V TGAGCTTGTG ACTCGAACAC S K D CTCCAAAGAT GAGGTTTCTA	TCCAGGGACA AGGTCCCTGT T K R E ACAAAGAGGG TGTTTCTCCC I L Q R ATTCTGCAGC TAAGACGTCG A I I A GCCATCATTG CGGTAGTAAC A K K Q GCCAAGAAAC CGGTTCTTTG L D L L
481 +3 541 +3 601 +3 661 +3 721	CAATCACAGA GTTAGTGTCT .I D F L TTGATTTTCT AACTAAAAGA .E D L V AAGACTTGGT TTCTGAACCA .R S K K GCAGCAAGAA CGTCGTTCTT .A R I D CCCGGACAGA GGGCCTGTCT .Q L L C	CACAGGCCGG GTGTCCGGCC K E E CAAAGAGGAG GTTTCTCCTC V A P GGTAGCCCT CCATCGGGGA G K L GGGAAAGTTG CCCTTTCAAC L K K CCTGAAGAAC GGACTTCTTC G A A	ATGGGGAGCC TACCCTCGG E H D GAACATGACT CTTGTACTGA A G ! GCAGGCATCA CGTCCGTAGT P ! V CCCATTGTAA GGGTAACATT N R D AATCGGGACT TTAGCCCTGA ! G T ATTGGCACTC	GCTTGGTGGG CGAACCACCC C F L E GTTTCTTGGA CAAAGAACCT T L K E CACTGAAGGA GTGACTTCCT N E D E ATGAAGATGA TACTTCTACT Y P L A ACCCACTAGC TGGGTGATCG H E D E ATGAGGATGA	CATCATCTCC GTAGTAGAGG E   M  AGAGATAATG TCTCTATTAC A N E GGCAAATGAA CCGTTTACTT E L V  TGAGCTTGTG ACTCGAACAC S K D  CTCCAAAGAT GAGGTTTCTA K Y R  CAAGTATAGG	TCCAGGGACA AGGTCCCTGT T K R E ACAAAGAGGG TGTTTCTCCC I L Q R ATTCTGCAGC TAAGACGTCG A I I A GCCATCATTG CGGTAGTAAC A K K Q GCCAAGAAAC CGGTTCTTTG L D L L CTGGACTTGC
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481 +3 541 +3 601 +3 661 +3 721 +3	CAATCACAGA GTTAGTGTCT .I D F L TTGATTTTCT AACTAAAAGA .E D L V AAGACTTGGT TTCTGAACCA .R S K K GCAGCAAGAA CGTCGTTCTT .A R I D CCCGGACAGA GGGCCTGTCT .O L L C AGCTGCTGTG TCGACGACAC	CACAGGCCGG GTGTCCGGCC K E E CAAAGAGGAG GTTTCTCCTC V A P GGTAGCCCCT CCATCGGGGA G K L GGGAAAGTTG CCCTTTCAAC L K K CCTGAAGAAC GGACTTCTTC G A A TGGGGGCAGCC ACCCGTCGG	ATGGGGAGCC TACCCCTCGG E H D GAACATGACT CTTGTACTGA A G ! GCAGGCATCA CGTCCGTAGT P ! V CCCATTGTAA GGGTAACATT N R D AATCGGGACT TTAGCCCTGA ! G T ATTGGCACTC TAACCGTGAG V V V	GCTTGGTGGG CGAACCACCC C F L E GTTTCTTGGA CAAAGAACCT T L K E CACTGAAGGA GTGACTTCCT N E D C ATGAAGATGA TACTTCTACT Y P L A ACCCACTAGC TGGGTGATCG H E D C ATGAGGATGA TACTCCTACT L D S E	CATCATCTCC GTAGTAGAGG E   M  AGAGATAATG TCTCTATTAC A N E  GGCAAATGAA CCGTTTACTT E L V  TGAGCTTGTG ACTCGAACAC S K D  CTCCAAAGAT GAGGTTTCTA K Y B  CAAGTATAGG GTTCATATCC Q G N	TCCAGGGACA AGGTCCCTGT T K R E ACAAAGAGGG TGTTTCTCCC I L Q R ATTCTGCAGC TAAGACGTCG A I I A GCCATCATTG CGGTAGTAAC A K K Q GCCAAGAAAC CGGTTCTTTG L D L L CTGGACTTGC GACCTGAACG S I F Q
481 +3 541 +3 601 +3 661 +3 721 +3 781	CAATCACAGA GTTAGTGTCT .I D F L TTGATTTTCT AACTAAAAGA .E D L V AAGACTTGGT TTCTGAACCA .R S K K GCAGCAAGAA CGTCGTTCTT .A R I D CCCGGACAGA GGGCCTGTCT .Q L L C AGCTGCTGTG TCGACGACAC .L A Q A	CACAGGCCGG GTGTCCGGCC K E E CAAAGAGGAG GTTTCTCCTC V A P GGTAGCCCCT CCATCGGGGA G K L GGGAAAGTTG CCCTTTCAAC L K K CCTGAAGAAC GGACTTCTTC G A A TGGGGCAGCC ACCCGTCGG G V D	ATGGGGAGCC TACCCCTCGG E H D GAACATGACT CTTGTACTGA A G ! GCAGGCATCA CGTCCGTAGT P ! V CCCATTGTAA GGGTAACATT N R D AATCGGGACT TTAGCCCTGA ! G T ATTGGCACTC TAACCGTGAG V V V CTAGTGGTTT	GCTTGGTGGG CGAACCACCC C F L E GTTTCTTGGA CAAAGAACCT T L K E CACTGAAGGA GTGACTTCCT N E D E ATGAAGATGA TACTTCTACT Y P L A ACCCACTAGC TGGGTGATCG H E D C ATGAGGATGA TACTCCTACT L D S E	CATCATCTCC GTAGTAGAGG E   M  AGAGATAATG TCTCTATTAC A N E  GGCAAATGAA CCGTTTACTT E L V  TGAGCTTGTG ACTCGAACAC S K D  CTCCAAAGAT GAGGTTTCTA K Y B  CAAGTATAGG GTTCATATCC Q G N  CCAGGGAAAT	TCCAGGGACA AGGTCCCTGT I K R E ACAAAGAGGG TGTTTCTCCC I L Q R ATTCTGCAGC TAAGACGTCG A I I A GCCATCATTG CGGTAGTAAC A K K Q GCCAAGAAAC CGGTTCTTTG L D L L CTGGACTTGC GACCTGAACG S I F Q TCCATCTTCC
481 +3 541 +3 601 +3 661 +3 721 +3 781 +3	CAATCACAGA GTTAGTGTCT  I D F L  TTGATTTTCT AACTAAAAGA  E D L V  AAGACTTGGT  TTCTGAACCA  R S K K  GCAGCAAGAA  CGTCGTTCTT  A R I D  CCCGGACAGA  GGGCCTGTCT  O L L C  AGCTGCTGTG  TCGACGACAC  L A Q A  TCGCCCAGGC  AGCGGGTCCG	CACAGGCCGG GTGTCCGGCC K E E CAAAGAGGAG GTTTCTCCTC V A P GGTAGCCCCT CCATCGGGGA G K L GGGAAAGTTG CCCTTTCAAC L K K CCTGAAGAAC GGACTTCTTC G A A TGGGGCAGCC ACCCCGTCGG G V D TGGTGTGGAT	ATGGGGAGCC TACCCCTCGG E H D GAACATGACT CTTGTACTGA A G ! GCAGGCATCA CGTCCGTAGT P ! V CCCATTGTAA GGGTAACATT N R D AATCGGGACT TTAGCCCTGA ! G T ATTGGCACTGA V V V GTAGTGGTTT CATCACCAAA	GCTTGGTGGG CGAACCACCC C F L E GTTTCTTGGA CAAAGAACCT T L K E CACTGAAGGA GTGACTTCCT N E D E ATGAAGATGA TACTTCTACT Y P L A ACCCACTAGC TGGGTGATCG H E D E ATGAGGATGA TACTCCTACT L D S E TGGACTCTTC ACCTGAGAAG	CATCATCTCC GTAGTAGAGG E   M  AGAGATAATG TCTCTATTAC A N E GGCAAATGAA CCGTTTACTT E L V  TGAGCTTGTG ACTCGAACAC S K D  CTCCAAAGAT GAGGTTTCTA K Y R  CAAGTATAGG GTTCATATCC Q G N  CCAGGGAAAT GGTCCCTTTA	TCCAGGGACA AGGTCCTGT I K R E ACAAAGAGGG TGTTTCTCCC I L Q R ATTCTGCAGC TAAGACGTCG A I I A GCCATCATTG CGGTAGTAAC A K K Q GCCAAGAAAC CGGTTCTTTG L D L L CTGGACTTGC GACCTGAACG S I F Q TCCATCTTCC AGGTAGAAGG
481 +3 541 +3 601 +3 661 +3 721 +3 781 +3	CAATCACAGA GTTAGTGTCT .I D F L TTGATTTTCT AACTAAAAGA .E D L V AAGACTTGGT TTCTGAACCA .R S K K GCAGCAAGAA CGTCGTTCTT .A R I D CCCGGACAGA GGGCCTGTCT .Q L L C AGCTGCTGTG TCGACGACAC .L A Q A TCGCCCAGGC AGCGGGTCCG	CACAGGCCGG GTGTCCGGCC K E E CAAAGAGGAG GTTTCTCCTC V A P GGTAGCCCCT CCATCGGGGA G K L GGGAAAGTTG CCCTTTCAAC L K K CCTGAAGAAC GGACTTCTTC G A A TGGGGGCAGCC ACCCCGTCGG G V D TGGTGTGGAT ACCACCCTA	ATGGGGAGCC TACCCTCGG E H D GAACATGACT CTTGTACTGA A G ! GCAGGCATCA CGTCCGTAGT P ! V CCCATTGTAA GGGTAACATT N R D AATCGGGACT TTAGCCCTGA ! G T ATTGGCACTCA CTAACCGTGAG V V V CGTAGTGGTTT CATCACCAAA I K D	GCTTGGTGGG CGAACCACCC C F L E GTTTCTTGGA CAAAGAACCT T L K E CACTGAAGGA GTGACTTCCT N E D E ATGAAGATGA TACTTCTACT Y P L A ACCCACTAGC TGGGTGATCG H E D E ATGAGGATGA TACTCCTACT L D S E TGGACTCTTC ACCTGAGAAG K Y P	CATCATCTCC GTAGTAGAGG E   M  AGAGATAATG TCTCTATTAC A N E GGCAAATGAA CCGTTTACTT E L V  TGAGCTTGTG ACTCGAACAC S K D CTCCAAAGAT GAGGTTTCTA K Y R CAAGTATAGG GTTCATATCC Q G N CCAGGGAAAT GGTCCCTTTA	TCCAGGGACA AGGTCCCTGT T K R E ACAAAGAGGG TGTTTCTCCC I L Q R ATTCTGCAGC TAAGACGTCG A I I A GCCATCATTG CGGTAGTAAC A K K Q GCCAAGAAAC CGGTTCTTTG L D L L CTGGACTTGC GACCTGAACG S I F Q TCCATCATTCC AGGTAGAAGG I G G N
481 +3 541 +3 601 +3 661 +3 721 +3 781 +3 841	CAATCACAGA GTTAGTGTCT .I D F L TTGATTTTCT AACTAAAAGA .E D L V AAGACTTGGT TTCTGAACCA .R S K K GCAGCAAGAA CGTCGTTCTT .A R I D CCCGGACAGA GGGCCTGTCT .Q L L C AGCTGCTGTG TCGACGACAC .L A Q A TCGCCCAGGC AGCCGGTCCG .Q I N M	CACAGGCCGG GTGTCCGGCC K E E CAAAGAGGAG GTTTCTCCTC V A P GGTAGCCCCT CCATCGGGGA G K L GGGAAAGTTG CCCTTTCAAC L K K CCTGAAGAAC GGACTTCTTC G A A TGGGGCAGCC ACCCGTCGG G V D TGGTGTGGAT ACCACACCTA	ATGGGGAGCC TACCCTCGG E H D GAACATGACT CTTGTACTGA A G ! GCAGGCATCA CGTCCGTAGT P ! V CCCATTGTAA GGGTAACATT N R D AATCGGGACT TTAGCCCTGA ! G T ATTGGCACTGA V V V GTAGTGGTTT CATCACCAAA ! K D	GCTTGCTGGG CGAACCACCC C F L E GTTTCTTGGA CAAAGAACCT T L K E CACTGAAGGA GTGACTTCCT N E D E ATGAAGATGA TACTTCTACT Y P L A ACCCACTAGC TGGGTGATCG H E D E ATGAGGATGA TACTCCTACT L D \$ E TGGACTCTTC ACCTGAGAAG K Y P	CATCATCTCC GTAGTAGAGG E   M  AGAGATAATG TCTCTATTAC A N E  GGCAAATGAA CCGTTTACTT E L V  TGAGCTTGTG ACTCGAACAC S K D  CTCCAAAGAT GAGGTTTCTA K Y R  CAAGTATAGG GTTCATATCC Q G N  CCAGGGAAAT GGTCCCTTTA L Q V  TCTCCAAGTC	TCCAGGGACA AGGTCCCTGT T K R E ACAAAGAGGG TGTTTCTCCC I L Q R ATTCTGCAGC TAAGACGTCG A I I A GCCATCATTG CGGTAGTAAC A K K Q GCCAAGAAAC CGGTTCTTTG L D L L CTGGACTTGC GACCTGAACG S I F Q TCCATCTTCC AGGTAGAAGG I G G N ATTGGAGGCA
481 +3 541 +3 601 +3 661 +3 721 +3 781 +3 841 +3	CAATCACAGA GTTAGTGTCT .I D F L TTGATTTTCT AACTAAAAGA .E D L V AAGACTTGGT TTCTGAACCA .R S K K GCAGCAAGAA CGTCGTTCTT .A R I D CCCGGACAGA GGGCCTGTCT .Q L L C AGCTGCTGTG TCGACGACAC .L A Q A TCGCCCAGGC AGCCGGTCCG .Q I N M	CACAGGCCGG GTGTCCGGCC K E E CAAAGAGGAG GTTTCTCCTC V A P GGTAGCCCCT CCATCGGGGA G K L GGGAAAGTTG CCCTTTCAAC L K K CCTGAAGAAC GGACTTCTTC G A A TGGGGCAGCC ACCCGTCGG G V D TGGTGTGGAT ACCACACCTA	ATGGGGAGCC TACCCTCGG E H D GAACATGACT CTTGTACTGA A G ! GCAGGCATCA CGTCCGTAGT P ! V CCCATTGTAA GGGTAACATT N R D AATCGGGACT TTAGCCCTGA ! G T ATTGGCACTGA V V V GTAGTGGTTT CATCACCAAA ! K D	GCTTGCTGGG CGAACCACCC C F L E GTTTCTTGGA CAAAGAACCT T L K E CACTGAAGGA GTGACTTCCT N E D E ATGAAGATGA TACTTCTACT Y P L A ACCCACTAGC TGGGTGATCG H E D E ATGAGGATGA TACTCCTACT L D \$ E TGGACTCTTC ACCTGAGAAG K Y P	CATCATCTCC GTAGTAGAGG E   M  AGAGATAATG TCTCTATTAC A N E  GGCAAATGAA CCGTTTACTT E L V  TGAGCTTGTG ACTCGAACAC S K D  CTCCAAAGAT GAGGTTTCTA K Y R  CAAGTATAGG GTTCATATCC Q G N  CCAGGGAAAT GGTCCCTTTA L Q V  TCTCCAAGTC	TCCAGGGACA AGGTCCCTGT T K R E ACAAAGAGGG TGTTTCTCCC I L Q R ATTCTGCAGC TAAGACGTCG A I I A GCCATCATTG CGGTAGTAAC A K K Q GCCAAGAAAC CGGTTCTTTG L D L L CTGGACTTGC GACCTGAACG S I F Q TCCATCATTCC AGGTAGAAGG I G G N

HELLER EHRMAN WHITE & MCAULIFFE LLP

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### **SELECTION SYSTEMS FOR GENETICALLY** MODIFIED CELLS



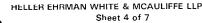


## SELECTION SYSTEMS FOR GENETICALLY MODIFIED CELLS

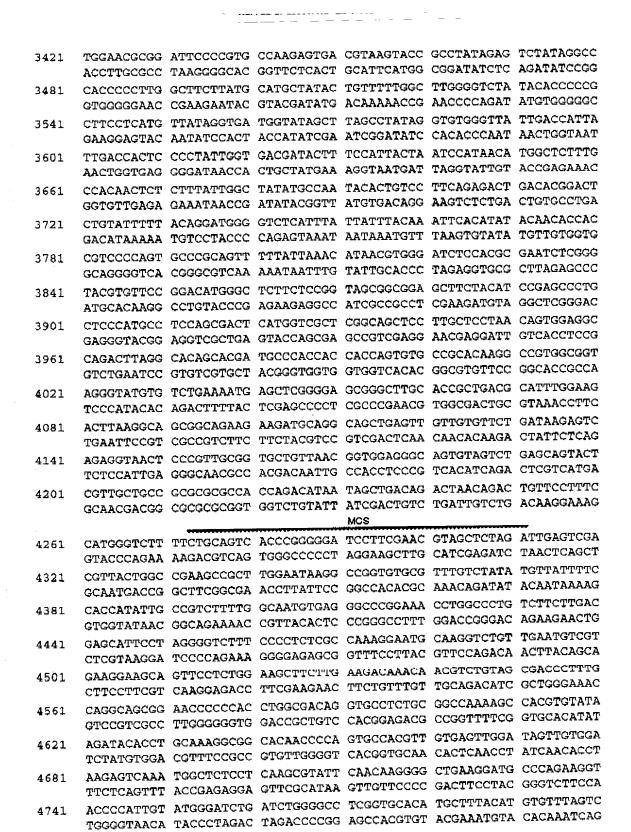
DOCKET NO. 24751-2502 Applicant: Jensen



					0.00001.00001	m
2041	CTGGAAGCTC	CCTCGTGCGC	TCTCCTGTTC	CGACCCTGCC	GCTTACCGGA	AMCGACAGGC
		GGAGCACGCG				
2101	CCTTTCTCCC	TTCGGGAAGC AAGCCCTTCG	GTGGCGCTTT	CACTTACCAC	TGCGACATCC	ATAGAGTCAA
	GGAAAGAGGG	CGTTCGCTCC	AAADOOOOO	CHCHCCYCCY	ACCCCCCCCCTTT	CAGCCCGACC
2161	CGGTGTAGGT	GCAAGCGAGG	MAGCIGGGCI	CACACGTGCT	TGGGGGGCAA	GTCGGGCTGG
	GCCACATCCA	ATCCGGTAAC	TICGNOCCON	AGTOCAACCC	CCTAACACAC	GACTTATCGC
2221	GCTGCGCCTT	TAGGCCATTG	ATAGCAGAAC	TCAGGTTGGG	CCATTCTGTG	CTGAATAGCG
2201		AGCCACTGGT				
2281	CACIGGCAGC	TCGGTGACCA	TTGTCCTAAT	CGTCTCGCTC	CATACATCCG	CCACGATGTC
2241		GTGGTGGCCT				
2341	TCAAGAACTT	CACCACCGGA	TTGATGCCGA	TGTGATCTTC	TTGTCATAAA	CCATAGACGC
2401	СТСТССТСАА	GCCAGTTACC	TTCGGAAAAA	GAGTTGGTAG	CTCTTGATCC	GGCAAACAAA
2401	GAGACGACTT	CGGTCAATGG	AAGCCTTTTT	CTCAACCATC	GAGAACTAGG	CCGTTTGTTT
2461	CCACCGCTGG	TAGCGGTGGT	TTTTTTGTTT	GCAAGCAGCA	GATTACGCGC	AGAAAAAAAG
****	GGTGGCGACC	ATCGCCACCA	ААААААСААА	CGTTCGTCGT	CTAATGCGCG	TCTTTTTTTC
2521	GATOTOAAGA	AGATCCTTTG	ATCTTTTCTA	CGGGGTCTGA	CGCTCAGTGG	AACGAAAACT
2 32 1	CTAGAGTTCT	TCTAGGAAAC	TAGAAAAGAT	GCCCCAGACT	GCGAGTCACC	TTGCTTTTGA
2581	САССТТААСС	GATTTTGGTC	ATGGCTAGTT	AATTAAGCTG	CAATAAACAA	TCATTATTTT
7.4	GTGCAATTCC	CTAAAACCAG	TACCGATCAA	${\tt TTAATTCGAC}$	GTTATTTGTT	AGTAATAAAA
2641	САФФССАФСФ	GTGTGTTGGT	TTTTTGTGTG	GCCTTGGGGG	AGGGGGAGGC	CAGAATGACT
	GTAACCTAGA	CACACAACCA	AAAAACACAC	CCGAACCCCC	TCCCCCTCCG	GTCTTACTGA
2701	CCAAGAGCTA	CAGGAAGGCA	GGTCAGAGAC	CCCACTGGAC	AAACAGTGGC	TGGACTCTGC
	GGTTCTCGAT	GTCCTTCCGT	CCAGTCTCTG	GGGTGACCTG	TTTGTCACCG	ACCTGAGACG
2761	ACCATAACAC	ACAATCAACA	GGGGAGTGAG	CTGGATCGAG	CTAGAGTCCG	TTACATAACT
	TGGTATTGTG	TGTTAGTTGT	CCCCTCACTC	GACCTAGCTC	GATCTCAGGC	AATGTATTGA
2821	TACGGTAAAT	GGCCCGCCTG	GCTGACCGCC	CAACGACCCC	CGCCCATTGA	CGTCAATAAT
	ATGCCATTTA	CCGGGCGGAC	CGACTGGCGG	GTTGCTGGGG	GCGGGTAACT	GCAGTTATTA
2881	GACGTATGTŢ	CCCATAGTAA	CGCCAATAGG	GACTTTCCAT	TGACGTCAAT	GGGTGGAGTA
	CTGCATACAA	GGGTATCATT	GCGGTTATCC	CTGAAAGGTA	ACTGCAGTTA	CCCACCTCAT
2941	TTTACGGTAA	ACTGCCCACT	TGGCAGTACA	TCAAGTGTAT	CATATGCCAA	GTACGCCCCC
	AAATGCCATT	TGACGGGTGA	ACCGTCATGT	AGTTCACATA	GTATACGGTT	CA1GCGGGGG
3001	TATTGACGTC	AATGACGGTA	AATGGCCCGC	CTGGCATTAT	GCCCAGTACA CCCCAGTACA	ACTEGAATAC
	ATAACTGCAG	TTACTGCCAT	TTACCGGGCG	GACCGTAATA	CGGGTCAIGI	MCCMC ATCCC
3061	GGACTTTCCT	ACTTGGCAGT	ACATCTACGT	ATTAGTCATC	CCATATACCA	ACCACTACGC
	CCTGAAAGGA	TGAACCGTCA	TGTAGATGCA	TAATCAGIAG	mexecces m	TTCCA AGTCT
3121	GTTTTGGCAG	TACATCAATG ATGTAGTTAC	GGCGTGGATA	GCGGTTTGAC	AGTGCCCCTA	AAGGTTCAGA
	CAAAACCGTC	GACGTCAATG	CCGCACCIA	mmhara arca a	AATCAACGGG	ACTTTCCAAA
3181	CCACCCCATT	GACGTCAATG CTGCAGTTAC	GGAGTTTGTT	A A C C C T G C T T	TTAGTTGCCC	TGAAAGGTTT
	GGTGGGGTAA	AACTCCGCCC	CCICARACAR	本本中に合合合合合の	AGGCGTGTAC	GGTGGGAGGT
3241	ATGTCGTAAC	AACTCCGCCC TTGAGGCGGG	CATTGACGCA	TTACCCGCCA	TCCGCACATG	CCACCCTCCA
	TACAGCATTG	TIGNGGCGGG	መአርጥር አልሮሮር	тсадатсясс	TGGAGACGCC	ATCCACGCTG
3301	CTATATAAGC	TOTO CONCORD	ATCACTTGGC	AGTCTAGCGG	ACCTCTGCGG	TAGGTGCGAC
		መመመለ ተመለጠ አር አር	A CCCCCCACCC	ATCCAGCCTC	CGCGGCCGGG	AACGGTGCAT
3361	TTTTGACCTC	CATAGAAGAC CMAMCMMCMC	TGGCCCTGGC	TAGGTCGGAG	GCGCCGGCCC	TTGCCACGTA
	HUNDA'T ARMA	CIMICAL	= =			



### SELECTION SYSTEMS FOR GENETICALLY MODIFIED CELLS



## HELLER EHRMAN WHITE & MCAULIFFE LLP Sheet 5 of 7 SELECTION SYSTEMS FOR GENETICALLY MODIFIED CELLS

4801		AAACGTCTAG TTTGCAGATC				
		CATGGGTAAG				
4861	TGCTATTATG	GTACCCATTC	ACTATAGATG	ATCAACACTG	GCCGCGGATC	ACAACTGTTA
4921		CATAGTATAT GTATCATATA				
4981		AACCTTCTTC				
1301	CAGCTGATGA	TTGGAAGAAG	AGAAAGGATG	TCGACTCTAG	TGGCCATCCT	CCCGGTAGTA
5041		GAACTCACCG				
		CTTGAGTGGC				
5101		CTGATGCAGC				
		GACTACGTCG				
5161		GGATATGTCC				
		CCTATACAGG				
5221	TTATGTTTAT	CGGCACTTTG	CATCGGCCGC	GCTCCCGATT	CCGGAAGTGC	TTGACATTGG
		GCCGTGAAAC				
5281		GAGAGCCTGA				
•		CTCTCGGACT				
5341		GAAACCGAAC				
		CTTTGGCTTG				
5401	GATCGCTGCG	GCCGATCTTA	GCCAGACGAG	CGGGTTCGGC	CCATTCGGAC	CGCAAGGAAT
		CGGCTAGAAT				
5461	CGGTCAATAC	ACTACATGGC	GTGATTTCAT	ATGCGCGATT	GCTGATCCCC	ATGTGTATCA
		TGATGTACCG				
5521	CTGGCAAACT	GTGATGGACG	ACACCGTCAG	TGCGTCCGTC	GCGCAGGCTC	ACCUACUACO
		CACTACCTGC				
5581	GATGCTTTGG	GCCGAGGACT	GCCCCGAAGT	CCGGCACCTC	CACCACGCGG	TANACCCGAG
		CGGCTCCTGA				
5641	CAACAATGTC	CTGACGGACA GACTGCCTGT	ATGGCCGCAT	MACAGCGGTC	TALEGACIGGA TALEGACCT	CGCTCCGCTA
		TCCCAATACG				
5701	GTTCGGGGAT	TCCCAATACG ACGGTTATGC	#CCACCCAA	CATCITCTIC	ACCTCCGGCA	CCAACCGAAC
		CAGACGCGCT				
5761	TATGGAGCAG	CAGACGCGCT GTCTGCGCGA	MCANCOTCOC	CTCCCTAGGC	CTCGAACGTC	CTAGCGGCGC
		TATATGCTCC				
5821	GCTCCGGGCG	ATATACGAGG	CGTAACCAGA	ACTGGTTGAG	ATAGTCTCGA	ACCAACTGCC
F 0 0 1		GATGCAGCTT				
5881	CHATTICGAT	CTACGTCGAA	CCCGCGTCCC	AGCTACGCTG	CGTTAGCAGG	CTAGGCCTCG
5941	CCCCACTCTC	GGGCGTACAC	AAATCGCCCG	CAGAAGCGCG	GCCGTCTGGA	CCGATGGCTG
3341	GCCCTGACAG	CCCCCATCTC	TTTAGCGGGC	GTCTTCGCGC	CGGCAGACCT	GGCTACCGAC
6001	TATACA ACTO	GCGTCTGCGT	TCGACCAGGC	TGCGCGTTCT	CGCGGCCATA	GCAACCGACG
OOOT	ACATCTTCAG	CGCAGAÇÇCA	AGCTGGTCCG	ACGCGCAAGA	GCGCCGGTAT	CGTTGGCTGC
6061	<b>ም እ</b> ሮርርር ርርሞቸር	COCCCTCGCC	GGCAGCAAGA	AGCCACGGAA	GTCCGCCCGG	AGÇAGAAAAT
0001	ATGCCGCAAC	GCGGGAGCGG	CCGTCGTTCT	TCGGTGCCTT	CAGGCGGGCC	TCGTCTTTTA
6121	<i>ተ</i> ረተረ እርር ርጥል	<del>ሶ</del> ጥረራርረርርጥጥጥ	ATATAGACGG	TCCCCACGGG	ATGGGGAAAA	CCACCACCAC
~ <del></del>	CGGGTGCGAT	GACGCCCAAA	TATATCTGCC	AGGGGTGCCC	TACCCCTTTT	GGTGGTGGTG

# Sheet 6 of 7 SELECTION SYSTEMS FOR GENETICALLY MODIFIED CELLS DOCUMENT NO 24374 2502

6181		GTGGCCCTGG CACCGGGACC				
6241		GTGCTGGGGG CACGACCCCC				
6301		GGTGAGATAT				
		CCACTCTATA				
6361		ATGCCTTATG				
		TACGGAATAC				
6421		TCACATGCCC				
		AGTGTACGGG				
6481		CTGTGCTACC				
		GACACGATGG				
6541		TTCGTGGCCC				
		AAGCACCGGG				
6601		GAGGACAGAC				
		CTCCTGTCTG				
6661		GCTATGCTGG				
		CGATACGACC				
6721		CACTGCGGCG				
	CGCCATAGAC	GTCACGCCGC	CCAGCACCGC	CCTCCTGACC	CCTGTCGAAA	GCCCCTGCCG
6781	CGTGCCGCCC	CAGGGTGCCG	AGCCCCAGAG	CAACGCGGGC	CCACGACCCC	ATATCGGGGA
	GCACGGCGGG	GTCCCACGGC	TCGGGGTCTC	GTTGCGCCCG	GGTGCTGGGG	TATAGCCCCT
6841		ACCCTGTTTC				
	GTGCAATAAA	TGGGACAAAG	CCCGGGGGCT	CAACGACCGG	GGGTTGCCGC	TGGACATATT
6901	CGTGTTTGCC	TGGGCCTTGG	ACGTCTTGGC	CAAACGCCTC	CGTTCCATGC	ACGTCTTTAT
	GCACAAACGG	ACCCGGAACC	TGCAGAACCG	GTTTGCGGAG	GCAAGGTACG	TGCAGAAATA
6961	CCTGGATTAC	GACCAATCGC	CCGCCGGCTG	CCGGGACGCC	CTGCTGCAAC	TTACCTCCGG
	GGACCTAATG	CTGGTTAGCG	GGCGGCCGAC	GGCCCTGCGG	GACGACGTTG	AATGGAGGCC
7021	GATGGTCCAG	ACCCACGTCA	CCACCCCCGG	CTCCATACCG	ACGATATGCG	ACCTGGCGCG
	CTACCAGGTC	TGGGTGCAGT	GGTGGGGGCC	GAGGTATGGC	TGCTATACGC	TGGACCGCGC
7081	CACGTTTGCC	CGGGAGATGG	GGGAGGCTAA	CTGAGTCGAG	AATTCGCTAG	AGGGCCCTAT
	GTGCAAACGG	GCCCTCTACC	CCCTCCGATT	GACTCAGCTC	TTAAGCGATC	TCCCGGGATA
7141	TCTATAGTGT	CACCTAAATG	CTAGAGCTCG	CTGATCAGCC	TCGACTGTGC	CTTCTAGTTG
	AGATATCACA	GTGGATTTAC	GATCTCGAGC	GACTAGTCGG	AGCTGACACG	GAAGATCAAC
7201	CCAGCCATCT	GTTGTTTGCC	CCTCCCCCGT	GCCTTCCTTG	ACCCTGGAAG	GTGCCACTCC
. •	GGTCGGTAGA	CAACAAACGG	GGAGGGGGCA	CGGAAGGAAC	TGGGACCTTC	CACGGTGAGG
7261	CACTGTCCTT	TCCTAATAAA	ATGAGGAAAT	TGCATCGCAT	TGTCTGAGTA	GGTGTCATTC
, 202	GTGACAGGAA	AGGATTATTT	TACTCCTTTA	ACGTAGCGTA	ACAGACTCAT	CCACAGTAAG
7321	TATTCTGGGG	GGTGGGGTGG	GGCAGGACAG	CAAGGGGGAG	GATTGGGAAG	ACAATAGCAG
	ATAAGACCCC	CCACCCCACC	CCGTCCTGTC	GTTCCCCCTC	CTAACCCTTC	TGTTATCGTC
7381	GCATGCGCAG	GGCCCAATTG	CTCGAGCGGC	CGCAATAAAA	TATCTTTATT	TTCATTACAT
	CGTACGCGTC	CCGGGTTAAC	GAGCTCGCCG	$\tt GCGTTATTTT$	ATAGAAATAA	AAGTAATGTA
7441	CTGTGTGTTG	GTTTTTTGTG	TGAATCGTAA	CTAACATACG	CTCTCCATCA	AAACAAAACG
	GACACACAAC	CAAAAAACAC	ACTTAGCATT	GATTGTATGC	GAGAGGTAGT	TTTGTTTTGC
7501	AAACAAAACA	AACTAGCAAA	ATAGGCTGTC	CCCAGTGCAA	${\tt GTGCAGGTGC}$	CAGAACATTT
	TTTGTTTTGT	TTGATCGTTT	TATCCGACAG	GGGTCACGTT	$\mathtt{CACGTCCACG}$	GTCTTGTAAA



## HELLER EHRMAN WHITE & MCAULIFFE LLP Sheet 7 of 7

## SELECTION SYSTEMS FOR GENETICALLY MODIFIED CELLS



7561		GGATCTGCGA				
	GAGATAGCTT	CCTAGACGCT	AGCGAGGCCA	CGGGCAGTCA	CCCGTCTCGC	GTGTAGCGGG
7621		AGAAGTTGGG				
	TGTCAGGGGC	TCTTCAACCC	CCCTCCCCAG	CCGTTAACTT	GGCCACGGAT	CTCTTCCACC
7681	CGCGGGGTAA	ACTGGGAAAG	TGATGTCGTG	TACTGGCTCC	GCCTTTTTCC	CGAGGGTGGG
	GCGCCCCATT	TGACCCTTTC	ACTACAGCAC	ATGACCGAGG	CGGAAAAAGG	GCTCCCACCC
7741	GGAGAACCGT	ATATAAGTGC	AGTAGTCGCC	GTGAACGTTC	TTTTTCGCAA	CGGGTTTGCC
	CCTCTTGGCA	TATATTCACG	TCATCAGCGG	CACTTGCAAG	AAAAAGCGTT	GCCCAAACGG
7801		AGCTGAAGCT				
	CGGTCTTGTG	TCGACTTCGA	AGCTCCCCGA	GCGTAGAGAG	GAAGTGCGCG	GGCGGCGGGA
7861		GCCATCCACG				
	TGGACTCCGG	CGGTAGGTGC	GGCCAACTCA	GCGCAAGACG	GCGGAGGGCG	GACACCACGG
7921	TCCTGAACTG	CGTCCGCCGT	CTAGGTAAGT	TTAAAGCTCA	GGTCGAGACC	GGGCCTTTGT
	AGGACTTGAC	GCAGGCGGCA	GATCCATTCA	AATTTCGAGT	CCAGCTCTGG	CCCGGAAACA
7981	CCGGCGCTCC	CTTGGAGCCT	ACCTAGACTC	${\tt AGCCGGCTCT}$	CCACGCTTTG	CCTGACCCTG
	GGCCGCGAGG	GAACCTCGGA	TGGATCTGAG	TCGGCCGAGA	GGTGCGAAAC	GGACTGGGAC
8041	CTTGCTCAAC	TCTACGTCTT	TGTTTCGTTT	TCTGTTCTGC	GCCGTTACAG	ATCCAAGCTG
	GAACGAGTTG	AGATGCAGAA	ACAAAGCAAA	AGACAAGACG	CGGCAATGTC	TAGGTTCGAC
8101		CTACGTAAGT	~*******			
	ACTGGCCGCG	GATGCATTCA	CTATAGATGA	TCTAAATAGT	TTTTCTCACA	ACTGAACACT
8161	GCGCTCACAA	TTGATACTTA	GATTCATCGA	GAGGGACACG	TCGACTACTA	ACCTTCTTCT
	CGCGAGTGTT	AACTATGAAT	CTAAGTAGCT	CTCCCTGTGC	AGCTGATGAT	TGGAAGAAGA
8221	CTTTCCTACA	GCTGAGAT				
	GAAAGGATGT	CGACTCTA				